



results of BLAST

BLASTN 2.2.9 [May-01-2004]

RID: 1095733595-30416-9286707536.BLASTQ4

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
2,600,233 sequences; 11,806,403,425 total letters

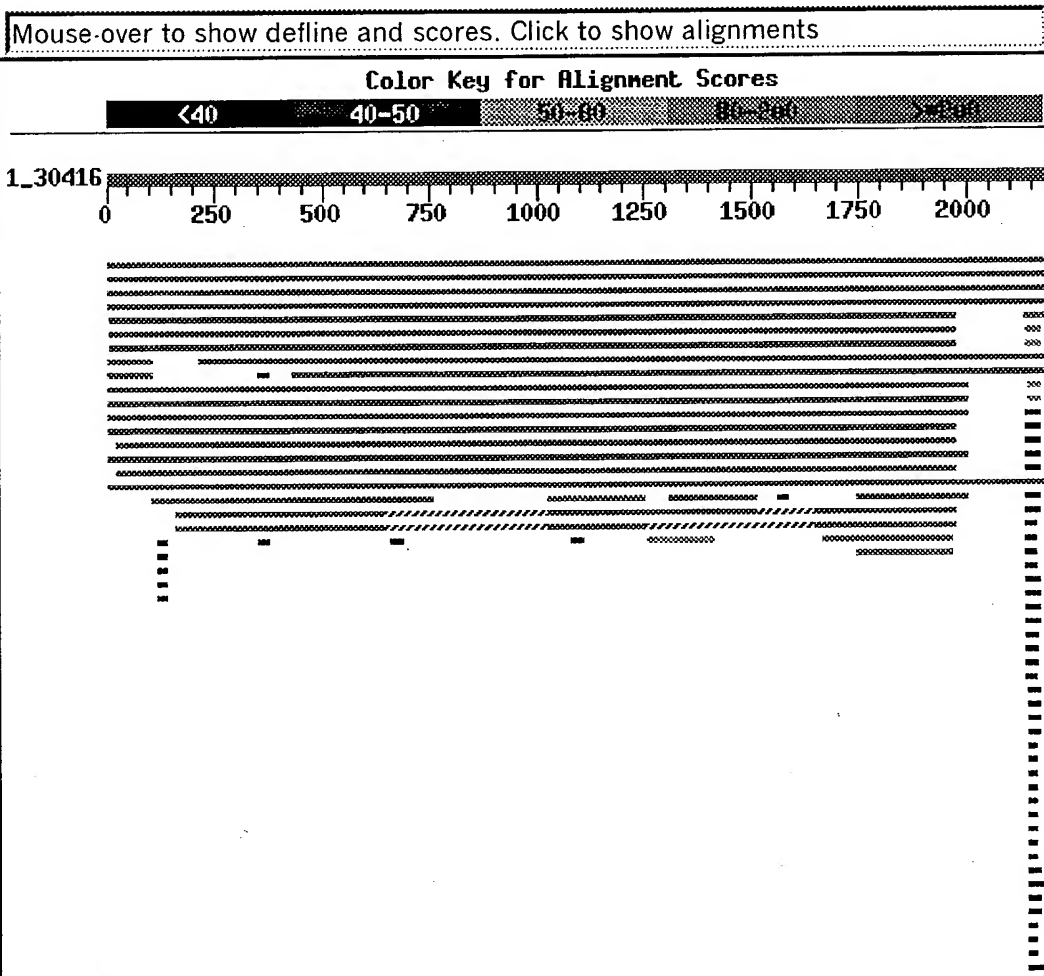
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)






































Query=

(2186 letters)

Distribution of 106 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Sequences producing significant alignments:			Score (bits)	E Value	
gi 34783298 gb BC017730.2	Homo sapiens tumor necrosis fact...	4180	0.0		
gi 7022799 dbj AK001504.1	Homo sapiens cDNA FLJ10642 fis, ...	4169	0.0		
gi 37181727 gb AY358304.1	Homo sapiens clone DNA52594 DR6-...	4163	0.0		
gi 23238206 ref NM_014452.3	Homo sapiens tumor necrosis fa...	4163	0.0		
gi 3549262 gb AF068868.1	Homo sapiens TNFR-related death r...	3784	0.0		
gi 30583678 gb BT007420.1	Homo sapiens tumor necrosis fact...	3784	0.0		
gi 32880108 gb BT009883.1	Synthetic construct Homo sapiens...	3780	0.0		
gi 17066395 emb AJ420531.1 HSA420531	Homo sapiens mRNA full...	3724	0.0		
gi 16507812 gb BC010241.1	Homo sapiens tumor necrosis fact...	3350	0.0		
gi 16741136 gb BC016420.1	Mus musculus tumor necrosis fact...	2363	0.0		
gi 31341673 ref NM_178589.2	Mus musculus tumor necrosis fa...	2357	0.0		
gi 26335926 dbj AK043823.1	Mus musculus 10 days neonate co...	2357	0.0		
gi 34874517 ref XM_236992.2	Rattus norvegicus similar to d...	2334	0.0		
gi 15020325 gb AY043489.1	Mus musculus death receptor 6 mR...	2329	0.0		
gi 26329206 dbj AK033529.1	Mus musculus adult male colon c...	2325	0.0		
gi 11559849 gb AF322069.1 AF322069	Mus musculus DR6 mRNA, c...	2317	0.0		
gi 10437705 dbj AK025235.1	Homo sapiens cDNA: FLJ21582 fis...	1258	0.0		
gi 6478163 emb AL096801.18 HSJ181J13	Human DNA sequence fro...	1258	0.0		
gi 14043014 gb AF349908.2 AF349908	Gallus gallus death rece...	448	e-122		
gi 50745307 ref XM_420067.1	PREDICTED: Gallus gallus simil...	344	4e-91		
gi 26085539 dbj AK036984.1	Mus musculus adult female vagin...	321	3e-84		
gi 17105105 gb AF432512.1 AF432512	Gallus gallus death rece...	206	2e-49		
gi 15880636 emb AJ336218.1 HSA336218	Homo sapiens genomic s...	196	1e-46		
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gi 41392831 emb BX842240.3	Zebrafish DNA sequence from clo...	133	2e-27		
gi 35209093 emb BX072534.9	Zebrafish DNA sequence from clo...	133	2e-27		
gi 13528779 gb BC005192.1	Homo sapiens tumor necrosis fact...	89	4e-14		
gi 45433459 emb BX511269.12	Zebrafish DNA sequence from cl...	87	1e-13		
gi 50299968 emb CR385023.7	Zebrafish DNA sequence from clo...	62	5e-06		
gi 20068779 emb AL672310.3	Human DNA sequence from clone R...	56	3e-04		
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gi 22475753 gb AC121844.2	Mus musculus BAC clone RP24-81L3...	45	0.77		
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gi 33620844 gb AC108838.20	Mus musculus chromosome 18, clo...	43	2.9
gi 51948684 gb AC139225.10	Mus musculus chromosome 9, clon...	43	2.9
gi 31745195 gb AC140862.3	Homo sapiens chromosome 16 clone...	43	2.9
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gi 27452920 gb AC016889.28	Homo sapiens chromosome 17, clo...	43	2.9
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gi 46576119 gb AC102312.11	Mus musculus chromosome 10, clo...	43	2.9
gi 15375118 gb AC008428.5	Homo sapiens chromosome 5 clone ...	43	2.9
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gi 24961407 gb AC096784.17	Mus musculus chromosome 10 clon...	43	2.9
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gi 34850546 gb AC114578.14	Mus musculus chromosome 19, clo...	43	2.9
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gi 34530170 dbj AK124394.1	Homo sapiens cDNA FLJ42403 fis,...	43	2.9
gi 9662953 emb AL359554.7	Human DNA sequence from clone RP...	43	2.9
gi 12053254 emb AL136875.1	HSM801843 Homo sapiens mRNA; cDN...	43	2.9
gi 20521915 dbj AB037853.2	Homo sapiens mRNA for KIAA1432 ...	43	2.9

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|34783298|gb|BC017730.2|  Homo sapiens tumor necrosis factor receptor superfamily class 1 member 1 mRNA (cDNA clone MGC:21476 IMAGE:3847246), complete cds
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Score = 4180 bits (2174), Expect = 0.0
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 Strand = Plus / Plus

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 Identities = 2076/2186 (94%)
 Strand = Plus / Plus

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|||||

[illegible]

Query: 2101 nnnnnnnnnnnnttaacagagaaaatgggcagtgcttgaattctttctccttctctct 2160

Query: 2161 ctcnnnnnnnnnnnaaataactcctct 2186
||| ||||| |||

☒ >gi|37181727|gb|AY358304.1| Homo sapiens clone DNA52594 DR6-TNFR (UNQ437) mRNA
 Length = 3534

Score = 4163 bits (2165), Expect = 0.0
Identities = 2078/2188 (94%), Gaps = 2/2188 (0%)
Strand = Plus / Plus

Query: 1 tcagccatggggacctctccgagcagcagcaccgcctcgcctcctgcagccgcatcgcc 60
 |||
 |||

Query: 61 cgccgagccacagccacgatgatcgcgggctcccttctctgcttggattccttagcacc 120

Query: 121 accacagctcagccagaacagaaggcctcgaatctcattggcacataccgccatggtgac 180

Query: 181 cgtgccacgaggccaggtgctaacctgtgacaagtgtccagcaggaacctatgtctctgag 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Query: 241 cattgtaccaacacaaagcctgcgcgtctgcagcagttgcctgtggggacctttaccagg 300



Nucleotide

Protein

formatting

BLAST

Translations

Retrieve results for an
RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (655 letters)

Putative conserved domains have been detected, click on the image below for detailed results.



The request ID is 1095736920-8332-97655742182.BLASTQ4

Format! or **Reset!**

The results are estimated to be ready in 20 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment in HTML

Use new formatter ☐ Masking Character Default(X for protein, n for nucleotide) Masking Color Black

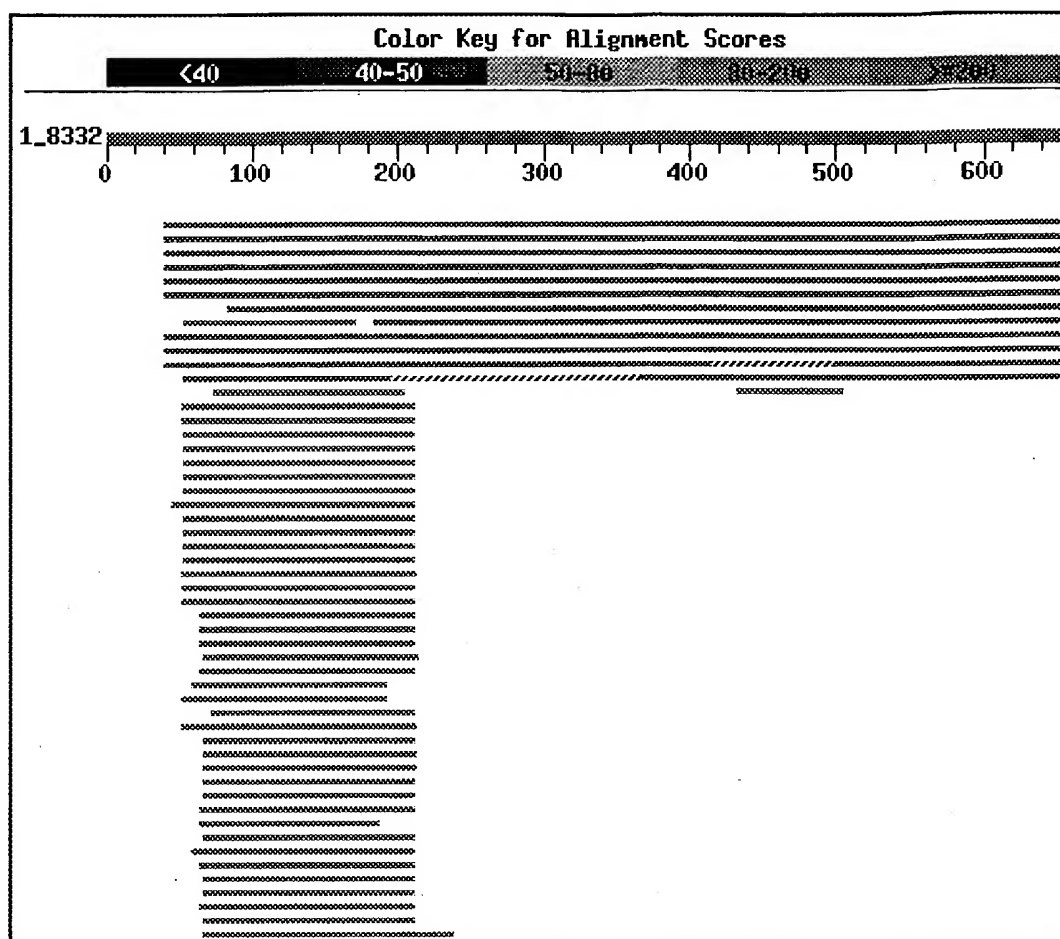
Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Format for PSI-BLAST ☐ with inclusion threshold: 0.005

Limit results by or select from: All organisms

Expect value range:



Sequences producing significant alignments:			Score (bits)	E Value	
gi 32880109 gb AAP88885.1	tumor necrosis factor receptor s...		1112	0.0	
gi 3549263 gb AAC34583.1	TNFR-related death receptor-6 [Ho...		1111	0.0	G
gi 16741137 gb AAH16420.1	Tumor necrosis factor receptor s...		993	0.0	G
gi 30519885 ref NP_848704.1	tumor necrosis factor receptor...		990	0.0	G
gi 34874518 ref XP_236992.2	similar to death receptor 6 [R...		984	0.0	G
gi 11559850 gb AAG38115.1	DR6 [Mus musculus]		982	0.0	G
gi 26329207 dbj BAC28342.1	unnamed protein product [Mus mu...		913	0.0	G
gi 16507813 gb AAH10241.1	TNFRSF21 protein [Homo sapiens]		820	0.0	G
gi 14043015 gb AAK29666.2	death receptor 6 [Gallus gallus]		755	0.0	
gi 25513801 pir JC7705	death receptor-6 - chicken		751	0.0	
gi 50745308 ref XP_420067.1	PREDICTED: similar to death re...		417	e-115	G
gi 47222484 emb CAG13004.1	unnamed protein product [Tetrao...		354	5e-96	
gi 15824372 gb AAL09310.1	death receptor 6 [Salvelinus fon...		166	1e-39	
gi 17105106 gb AAL35560.1	death receptor 6 [Gallus gallus]		142	3e-32	G
gi 14595071 emb CAC43329.1	putative decoy receptor 3 prote...		117	8e-25	
gi 15193279 gb AAK91758.1	TNF decoy receptor [Oncorhynchus...		117	8e-25	
gi 50731869 ref XP_418394.1	PREDICTED: similar to Tumor ne...		112	3e-23	G
gi 6981306 ref NP_037002.1	tumor necrosis factor receptor ...		109	2e-22	G
gi 38530117 gb AAR23265.1	tumor necrosis factor receptor s...		109	3e-22	G

gi 2072185 gb AAB53709.1	Human osteoprotegerin (OPG) prote...	109	3e-22	G
gi 20987350 gb AAH30155.1	Osteoprotegerin, precursor [Homo...	109	3e-22	G
gi 49256346 gb AAH74428.1	MGC84670 protein [Xenopus laevis]	108	4e-22	G
gi 6636399 gb AAF20168.1	osteoprotegerin [Homo sapiens]	108	4e-22	G
gi 31543882 ref NP_032790.2	tumor necrosis factor receptor...	107	9e-22	G
gi 37574033 gb AAH49782.1	Tumor necrosis factor receptor s...	107	1e-21	G
gi 21264085 sp O08712 T11B MOUSE	Tumor necrosis factor rece...	104	7e-21	G
gi 5924059 gb AAD56428.1	decoy TNF receptor [Salvelinus fo...	103	2e-20	
gi 50758825 ref XP_417434.1	PREDICTED: similar to decoy re...	103	2e-20	G
gi 21706465 gb AAH34349.1	TNFRSF6B protein [Homo sapiens] ...	100	8e-20	G
gi 4507577 ref NP_001057.1	tumor necrosis factor receptor ...	97	1e-18	G
gi 339758 gb AAA36755.1	tumor necrosis factor receptor	97	1e-18	G
gi 13236879 gb AAB19824.2	tumor necrosis factor receptor; ...	96	2e-18	G
gi 47221569 emb CAF97834.1	unnamed protein product [Tetrao...	96	3e-18	
gi 37359212 gb AAN72434.1	soluble tumor necrosis factor re...	96	4e-18	G
gi 51869972 ref YP_073525.1	tumor necrosis factor receptor...	95	5e-18	G
gi 30016907 gb AAP03889.1	decoy receptor 3 [Gallus gallus]	92	6e-17	G
gi 33873868 gb AAH11844.1	TNFRSF1B protein [Homo sapiens] ...	89	4e-16	G
gi 45709939 gb AAH67712.1	LOC407674 protein [Danio rerio]	89	4e-16	G
gi 45383287 ref NP_989770.1	tumor necrosis factor receptor...	89	4e-16	G
gi 33325070 gb AAQ08183.1	herpes virus entry mediator [Mus...	88	6e-16	G
gi 30725810 ref NP_849262.1	tumor necrosis factor receptor...	88	6e-16	G
gi 32700005 gb AAP86653.1	CD40 [Canis familiaris] >gi 5095...	87	1e-15	G
gi 34873138 ref XP_345617.1	similar to tumor necrosis fact...	86	4e-15	G
gi 30016909 gb AAP03890.1	osteoprotegerin [Gallus gallus]	86	5e-15	G
gi 18447759 gb AAL68402.1	membrane protein CD40 [Ovis aries]	85	5e-15	G
gi 2738131 gb AAB94383.1	tumor necrosis factor receptor II...	85	5e-15	
gi 24850129 ref NP_733805.1	tumor necrosis factor receptor...	85	7e-15	G
gi 45383273 ref NP_989775.1	CD30 protein [Gallus gallus] >...	84	8e-15	G
gi 135963 sp P25119 TR1B MOUSE	Tumor necrosis factor recept...	84	9e-15	G
gi 24850125 ref NP_733802.1	tumor necrosis factor receptor...	84	1e-14	G
gi 34860707 ref XP_230854.2	similar to T-cell differentiat...	84	1e-14	G
gi 346667 pir A46476	B cell-associated surface molecule CD...	84	1e-14	
gi 2501232 sp Q28203 TNR5_BOVIN	Tumor necrosis factor recep...	84	1e-14	G
gi 6755829 ref NP_035741.1	tumor necrosis factor receptor ...	84	1e-14	G
gi 34499988 gb AAQ73576.1	tumor necrosis factor receptor I...	84	1e-14	
gi 267407 sp P29825 VT2_MYXVL	Tumor necrosis factor soluble...	84	2e-14	G
gi 2738067 gb AAB94361.1	tumor necrosis factor receptor II...	83	3e-14	
gi 2738073 gb AAB94364.1	tumor necrosis factor receptor II...	83	3e-14	
gi 2738083 gb AAB94367.1	tumor necrosis factor receptor II...	83	3e-14	
gi 17529970 gb AAL40648.1	J2R [Monkeypox virus] >gi 175297...	83	3e-14	G
gi 30519576 emb CAD90751.1	K3R protein [Cowpox virus]	82	4e-14	
gi 18056484 emb CAC83048.1	CrmE protein [Vaccinia virus]	82	4e-14	
gi 22137743 gb AAH29254.1	Tnfrsf5 protein [Mus musculus]	82	4e-14	G
gi 28875519 dbj BAC65226.1	tumor necrosis factor receptor-...	82	4e-14	
gi 2738127 gb AAB94381.1	tumor necrosis factor receptor II...	82	5e-14	
gi 2738069 gb AAB94362.1	tumor necrosis factor receptor II...	82	5e-14	
gi 2738087 gb AAB94369.1	tumor necrosis factor receptor II...	82	5e-14	
gi 2738071 gb AAB94363.1	tumor necrosis factor receptor II...	82	5e-14	

gi 47523466 ref NP_999359.1	CD40 [Sus scrofa] >gi 19697104...	81	7e-14	G
gi 2738065 gb AAB94360.1	tumor necrosis factor receptor II...	81	7e-14	
gi 47220788 emb CAF99995.1	unnamed protein product [Tetrao...	81	9e-14	
gi 6578689 gb AAF18043.1	s002R [Rabbit fibroma virus] >gi ...	80	2e-13	G
gi 24850121 ref NP_733803.1	tumor necrosis factor receptor...	80	2e-13	G
gi 4505039 ref NP_002333.1	lymphotoxin beta receptor; tumo...	80	2e-13	G
gi 2738089 gb AAB94370.1	tumor necrosis factor receptor II...	79	3e-13	
gi 11136919 emb CAC15562.1	CrmE protein [Cowpox virus]	79	3e-13	
gi 30519581 emb CAD90756.1	I4R protein [Cowpox virus] >gi ...	79	3e-13	
gi 32139918 emb CAD57165.1	tumour necrosis factor receptor...	79	3e-13	
gi 2738141 gb AAB94388.1	tumor necrosis factor receptor II...	79	4e-13	
gi 2738057 gb AAB94356.1	tumor necrosis factor receptor II...	79	5e-13	
gi 2738059 gb AAB94357.1	tumor necrosis factor receptor II...	79	5e-13	
gi 18483123 gb AAL73920.1	putative TNF receptor II CrmB; C...	79	5e-13	G
gi 9627717 ref NP_042240.1	G4R [Variola virus] >gi 516449 ...	79	5e-13	G
gi 2738135 gb AAB94385.1	tumor necrosis factor receptor II...	79	5e-13	
gi 2738103 gb AAB94377.1	tumor necrosis factor receptor II...	79	5e-13	
gi 2738101 gb AAB94376.1	tumor necrosis factor receptor II...	78	6e-13	
gi 2738137 gb AAB94386.1	tumor necrosis factor receptor II...	78	6e-13	
gi 5830759 emb CAB54798.1	G2R protein [Variola minor virus...	78	7e-13	
gi 2738099 gb AAB94375.1	tumor necrosis factor receptor II...	78	8e-13	
gi 2738093 gb AAB94372.1	tumor necrosis factor receptor II...	78	8e-13	
gi 885855 gb AAA69467.1	G2R [Variola virus] >gi 2738095 gb...	78	8e-13	
gi 2738139 gb AAB94387.1	tumor necrosis factor receptor II...	77	1e-12	
gi 50790945 ref XP_427848.1	PREDICTED: similar to osteopro...	77	1e-12	G
gi 2738143 gb AAB94389.1	tumor necrosis factor receptor II...	77	1e-12	
gi 333519 gb AAA60952.1	CrmB or CPXV005 protein [Cowpox vi...	77	2e-12	G
gi 30519575 emb CAD90750.1	K2R protein [Cowpox virus]	76	2e-12	
gi 2738145 gb AAB94390.1	tumor necrosis factor receptor II...	76	2e-12	
gi 2738055 gb AAB94355.1	tumor necrosis factor receptor II...	76	2e-12	
gi 2738129 gb AAB94382.1	tumor necrosis factor receptor II...	76	3e-12	
gi 433831 emb CAA53981.1	murine tumour necrosis factor rec...	75	5e-12	G

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|32880109|gb|AAP88885.1| tumor necrosis factor receptor superfamily, member 2
construct]
Length = 656

Score = 1112 bits (2875), Expect = 0.0

Identities = 560/615 (91%), Positives = 560/615 (91%)

Query: 41 AQPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHE 100
AQPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHE

Sbjct: 41 AQPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHE 100

Query: 101 NGIEKCHDCSQPCWPWMIKLPAAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKG 160
NGIEKCHDCSQPCWPWMIKLPAAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKG

Sbjct: 101 NGIEKCHDCSQPCWPWMIKLPAAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKG 160

Query: 161 TETEDVRCKQCARGTFSDVPSSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLXXXXXX 220

TETEDVRCKQCARGTFSDVPSSVMCKAYTDCLSQLVVIKPGTKETDNVCGTL
 Sbjct: 161 TETEDVRCKQCARGTFSDVPSSVMCKAYTDCLSQLVVIKPGTKETDNVCGTLPSFSSS 220

Query: 221 XXXXXGTAIFRPEHMETHEVFSSTYVPKGMNSTESNSSASVRPKVLSSIQEGTVPDNTS 280
 GTAIFRPEHMETHEV SSTYVPKGMNSTESNSSASVRPKVLSSIQEGTVPDNTS
 Sbjct: 221 TSPSPGTAIFRPEHMETHEVPSSTYVPKGMNSTESNSSASVRPKVLSSIQEGTVPDNTS 280

Query: 281 SARGKEDVNKTLPNLQVVNHQQGPHHRHILKLLPSMEATGGEKSSTPIKGPKRGHPRQNL 340
 SARGKEDVNKTLPNLQVVNHQQGPHHRHILKLLPSMEATGGEKSSTPIKGPKRGHPRQNL
 Sbjct: 281 SARGKEDVNKTLPNLQVVNHQQGPHHRHILKLLPSMEATGGEKSSTPIKGPKRGHPRQNL 340

Query: 341 HKHFDINEHLPWMXXXXXXXXXXXXXXXXXSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTP 400
 HKHFDINEHLPWM CSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTP
 Sbjct: 341 HKHFDINEHLPWMIVLFLLLVLVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTP 400

Query: 401 TQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAY 460
 TQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAY
 Sbjct: 401 TQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAY 460

Query: 461 AALQHWITIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQLETDKLALXXXXXXXXXX 520
 AALQHWITIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQLETDKLAL
 Sbjct: 461 AALQHWITIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQLETDKLALPMSPLSP 520

Query: 521 XXXXXNNAKLENSALLTVEPSPQDNKGFFVDESEPLLRCDXXXXXXXXXXXXXXFITKE 580
 NAKLENSALLTVEPSPQDNKGFFVDESEPLLRCDFITKE
 Sbjct: 521 SPIPSPNAKLENSALLTVEPSPQDNKGFFVDESEPLLRCSTSSGSSALSRNGSFITKE 580

Query: 581 KKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEAS 640
 KKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEAS
 Sbjct: 581 KKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEAS 640

Query: 641 QTL LDSVYSHLPDLL 655
 QTL LDSVYSHLPDLL
 Sbjct: 641 QTL LDSVYSHLPDLL 655

>gi|3549263|gb|AAC34583.1| [E] TNFR-related death receptor-6 [Homo sapiens]
 gi|37181728|gb|AAQ88671.1| [E] DR6-TNFR [Homo sapiens]
 gi|30583679|gb|AAP36088.1| [E] tumor necrosis factor receptor superfamily, member 2
 sapiens]
 gi|7657039|ref|NP_055267.1| [E] tumor necrosis factor receptor superfamily, member
 death receptor 6; TNFR-related death receptor 6 [Homo
 sapiens]
 gi|17389379|gb|AAH17730.1| [E] Tumor necrosis factor receptor superfamily, member 2
 [Homo sapiens]
 gi|21264087|sp|O75509|TR21_HUMAN [E] Tumor necrosis factor receptor superfamily mem
 (TNFR-related death receptor-6) (Death receptor 6)
 (UNQ437/PRO868)
 gi|7018385|emb|CAB75692.1| [E] dJ181J13.1 (Tumor necrosis factor receptor superfami
 (DR6)) [Homo sapiens]
 Length = 655

Score = 1111 bits (2874), Expect = 0.0
 Identities = 560/615 (91%), Positives = 560/615 (91%)

Query: 41 AQPEQKASNLIGTYRHVD RATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHE 100
 AQPEQKASNLIGTYRHVD RATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHE

Sbjct: 41 AQPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHE 100

Query: 101 NGIEKCHDCSQPCPWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKG 160
 NGIEKCHDCSQPCPWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKG

Sbjct: 101 NGIEKCHDCSQPCPWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKG 160

Query: 161 TETEDVRCKQCARGTFSVDPSSVMKCKAYTDCLSQLVVIKPGTKETDNVCGTLXXXXXX 220
 TETEDVRCKQCARGTFSVDPSSVMKCKAYTDCLSQLVVIKPGTKETDNVCGTL

Sbjct: 161 TETEDVRCKQCARGTFSVDPSSVMKCKAYTDCLSQLVVIKPGTKETDNVCGTLPSFSSS 220

Query: 221 XXXXXGTAIFRPRPEHMETHEVFSSTYVPGKMNSTESNSSASVRPKVLSSIQEGTVPDNTS 280
 GTAIFRPRPEHMETHEV SSTYVPGKMNSTESNSSASVRPKVLSSIQEGTVPDNTS

Sbjct: 221 TSPSPGTAIFRPRPEHMETHEVPSSTYVPGKMNSTESNSSASVRPKVLSSIQEGTVPDNTS 280

Query: 281 SARGKEDVNKTLPNLQVVNHQGGPHHRHILKLLPSMEATGGEKSSTPIKGPGRGHPRQNL 340
 SARGKEDVNKTLPNLQVVNHQGGPHHRHILKLLPSMEATGGEKSSTPIKGPGRGHPRQNL

Sbjct: 281 SARGKEDVNKTLPNLQVVNHQGGPHHRHILKLLPSMEATGGEKSSTPIKGPGRGHPRQNL 340

Query: 341 HKHFDINEHLPWMXXXXXXXXXXXXXXXXCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTP 400
 HKHFDINEHLPWM CSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTP

Sbjct: 341 HKHFDINEHLPWMIVLFLLLVLVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTP 400

Query: 401 TQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAY 460
 TQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAY

Sbjct: 401 TQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAY 460

Query: 461 AALQHWRTIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQLETDKLALXXXXXXXXXX 520
 AALQHWRTIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQLETDKLAL

Sbjct: 461 AALQHWRTIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQLETDKLALPMSPSPLSP 520

Query: 521 XXXXXNAKLENSALLTVEPSPQDKNKGFVDESEPLLRCDXXXXXXXXXXXXXXFITKE 580
 NAKLENSALLTVEPSPQDKNKGFVDESEPLLRC FITKE



Sbjct: 521 SPIPSPNAKLENSALLTVEPSPQDKNKGFVDESEPLLRCSTSSGSSALSRNGSFITKE 580

Query: 581 KKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIQAEDKLDRLFEIIGVKSQEAS 640
 KKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIQAEDKLDRLFEIIGVKSQEAS

Sbjct: 581 KKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIQAEDKLDRLFEIIGVKSQEAS 640

Query: 641 QTL LDSVYSHLPDLL 655
 QTL LDSVYSHLPDLL

Sbjct: 641 QTL LDSVYSHLPDLL 655

 >gi|16741137|gb|AAH16420.1|  Tumor necrosis factor receptor superfamily, member 1
 musculus]
 Length = 655

Score = 993 bits (2567), Expect = 0.0

Identities = 506/616 (82%), Positives = 520/616 (84%), Gaps = 2/616 (0%)

Query: 41 AQPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHE 100
 AQPEQK +L GTYRHVDR TGQVLTCDKCPAGTYVSEHCTN SLRVCSSCP GTFTTRHE

Sbjct: 41 AQPEQKTLSLPGTYRHVDRTTGQVLTCDKCPAGTYVSEHCTNMSLRVCSSCPAGTFTTRHE 100

Query: 101 NGIEKCHDCSQPCPWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKG 160
 NGIE+CHDCSQPCPWPMIE+LPCAALTDREC CPPGM+QSN TCAPHTVCPVGWGVRRKKG

Sbjct: 101 NGIERCHDCSQPCPWPMIERLPCAALTDRECICPPGMYQNGTCAPHTVCPVGWGVRRKKG 160

Query: 161 TETEDVRCKQCARGTFSVDPSSVMKCKAYTDCLSQLVVIKPGTKETDNVCGTLXXXXXX 220

TE EDVRCKQCARGTFSDVPSSVMKCKA+TDCL QNL V+KPGTKETDNVCG
 Sbjct: 161 TENEDVRCKQCARGTFSDVPSSVMKCKAHTDCLGQNLVVKPGTKETDNVCGMRLFFSST 220

Query: 221 XXXXXGTAIFPRPEHMETHEVFSSTYVPGKMNSTESNSSASVRPKVLSSIQEGTVPDNTS 280
 GT F PEHME+H+V SSTY P+GMNST+SNS+ASVR KV S I+EGTVPDNTS
 Sbjct: 221 NPPSSGTVTFSHPEHMESHVPSSTYEPQGMNSTDSNSTASVRTKVPSGIEEGTVPDNTS 280

Query: 281 SARGKEDVNKTLPLNLQVVNHQQGPHHRHILKLLP-SMEATGGEKSSTPIKGPGRGHPRQN 339
 S GKE N+TLPN V HQQ PHHRHILKLLP SMEAT GEKSST IK PKRGHPRQN
 Sbjct: 281 STSGKEGTNRTLPLNPPQVTHQQAPHHRHILKLLPSSMEAT-GEKSSTAIPKRGHPRQN 339

Query: 340 LHKHFDINEHLPWMXXXXXXXXXXXXXXXXCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMT 399
 HKHFDINEHLPWM CSIRKSSRTLKKGPRQDPSAIVEKAGLKKS+T
 Sbjct: 340 AHKHFDINEHLPWMIVLFLLLVLVLIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSIT 399

Query: 400 PTQNRKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERA 459
 PTQNRKWIYY NGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERA
 Sbjct: 400 PTQNRKWIYYRNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERA 459

Query: 460 YAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQLETDKLALXXXXXXXX 519
 YAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQLETDKLAL
 Sbjct: 460 YAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPSPLS 519

Query: 520 XXXXXXXNAKLENSALLTVEPSPQDNKNGFFVDESEPLLRCDXXXXXXXXXXXXXXFITK 579
 N KLENS LLTVEPSP DKNK FVDESEPLLRCDFITK
 Sbjct: 520 PSPIPSPNVKLENSTLLTVEPSPLDNKNCFFVDESEPLLRCSTSSGSSALSRNGSFITK 579

Query: 580 EKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEA 639
 EKKDTVLRQVRLDPCDLQPIFDDMLH LNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEA
 Sbjct: 580 EKKDTVLRQVRLDPCDLQPIFDDMLHILNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEA 639

Query: 640 SQTLLDSVYSHLPDLL 655
 SQTLLDSVYSHLPDLL
 Sbjct: 640 SQTLLDSVYSHLPDLL 655

>gi|30519885|ref|NP_848704.1| [G] tumor necrosis factor receptor superfamily, mem
 receptor 6; TNFR-related death receptor-6 [Mus musculus]
 gi|15020326|gb|AAK74193.1| [G] death receptor 6 [Mus musculus]
 gi|21264096|sp|Q9EPU5|TR21_MOUSE Tumor necrosis factor receptor superfamily membe
 (TNFR-related death receptor-6) (Death receptor 6)
 gi|26335927|dbj|BAC31664.1| [G] unnamed protein product [Mus musculus]
 Length = 655

Score = 990 bits (2559), Expect = 0.0

Identities = 506/616 (82%), Positives = 520/616 (84%), Gaps = 2/616 (0%)

Query: 41 AQPEQKASNLIGTYRHVDRTGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHE 100
 AQPEQK +L GTYRHVDR TGQVLTCDKCPAGTYVSEHCTN SLRVCSSCP GTFTTRHE
 Sbjct: 41 AQPEQKTLSPGTYRHVDRTGQVLTCDKCPAGTYVSEHCTNMSLRVCSSCPAGTFTTRHE 100

Query: 101 NGIEKCHDCSQPCPWPMMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKG 160
 NGIE+CHDCSQPCPWPMMIE+LPCAALTDREC CPPGM+QSN TCAPHTVCPVGWGVRRKKG
 Sbjct: 101 NGIERCHDCSQPCPWPMMIERLPCAALTDRECICPPGMYQSNGTAPHTVCPVGWGVRRKKG 160

Query: 161 TETEDVRCKQCARGTFSDVPSSVMKCKAYTDCLSQLNVVVKPGTKETDNVCGTLXXXXXX 220
 TE EDVRCKQCARGTFSDVPSSVMKCKA+TDCL QNL V+KPGTKETDNVCG
 Sbjct: 161 TENEDVRCKQCARGTFSDVPSSVMKCKAHTDCLGQNLVVKPGTKETDNVCGMRLFFSST 220

Query: 221 XXXXXGTAIFPRPEHMETHEVFSSTYVPKGMNSTESNSSASVRPKVLSSIQEGTVPDNTS 280
 GT F PEHME+H+V SSTY P+GMNST+SNS+ASVR KV S I+EGTVPDNTS
 Sbjct: 221 NPPSSGTVTFSHPEHMESHDPVSSTYEPQGMNSTDSNSTASVRTKVPKSGIEEGTVPDNTS 280

Query: 281 SARGKEDVNKTLPNLQVVNHQQGPHHRHILKLLP-SMEATGGEKSSTPIKGPGRGHPQRN 339
 S GKE N+TLPN V HQQ PHHRHILKLLP SMEAT GEKSST IK PKRGHPRQN
 Sbjct: 281 STSGKEGTNRNLTLPNPPQVTHQQAPHHRHILKLLPSSMEAT-GEKSSTAIKAPKRGHPRQN 339

Query: 340 LHKHFDINEHLPWMXXXXXXXXXXXXXCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSM 399
 HKHFDINEHLPWM CSIRKSSRTLKKGPRQDPSAIVEKAGLKKST
 Sbjct: 340 AHKHFDINEHLPWMIVLFLLLVLVLIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSLT 399



Query: 400 PTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERA 459
 PTQNREKWIYY NGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERA
 Sbjct: 400 PTQNREKWIYYRNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERA 459

Query: 460 YAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQLETDKLALXXXXXXXX 519
 YAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQLETDKLAL
 Sbjct: 460 YAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPSPLS 519

Query: 520 XXXXXXXXNAKLENSALLTVEPSPQDKNKGFVDESEPLLRCDXXXXXXXXXXXXXXFITK 579
 N KLENS LLTVEPSP DKNK FVDESEPLLRCDFITK
 Sbjct: 520 PSPMPSPNVKLENSLLTVEPSPLDKNKCFVDESEPLLRCDSSTSGSSALSRNGSFITK 579

Query: 580 EKKDVTLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEA 639
 EKKDVTLRQVRLDPCDLQPIFDDMLH LNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEA
 Sbjct: 580 EKKDVTLRQVRLDPCDLQPIFDDMLHILNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEA 639

Query: 640 SQTLLDSVYSHLPDLL 655
 SQTLLDSVYSHLPDLL
 Sbjct: 640 SQTLLDSVYSHLPDLL 655

 >gi|34874518|ref|XP_236992.2|  similar to death receptor 6 [Rattus norvegicus]
 Length = 655

Score = 984 bits (2545), Expect = 0.0
 Identities = 503/616 (81%), Positives = 520/616 (84%), Gaps = 2/616 (0%)

Query: 41 AQPEQKASNLIGTYRHVDRTGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHE 100
 AQPEQK +L GTYRHVDR TGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCP GTFTTRHE
 Sbjct: 41 AQPEQKTLSTLTGTYRHVDRTTGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPSGTFTTRHE 100

Query: 101 NGIEKCHDCSQPCPWPMEIKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKG 160
 NGIE+CHDCSQPCP PMIE+LPCAALTDREC CPPGM+QSN TCAPHTVCPVGWGVRRKKG
 Sbjct: 101 NGIERCHDCSQPCPRPMIERLPCAALTDRECICPPGMYQSNGTAPHTVCPVGWGVRRKKG 160

Query: 161 TETEDVRCKQCARGTFSDVPSSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLXXXXXX 220
 TE EDVRCKQCARGTFSDVPSSVMKC+A+TDCL QNL+V+K GTKETDNVCG
 Sbjct: 161 TENEDVRCKQCARGTFSDVPSSVMKCRAHTDCLGQNLMMVVKQGTKETDNVCGVHLSSSST 220

Query: 221 XXXXXGTAIFPRPEHMETHEVFSSTYVPKGMNSTESNSSASVRPKVLSSIQEGTVPDNTS 280
 G A F PEH E+H+V SSTY P+GMNST+SNS+ASVR KV S IQE TVPDNTS
 Sbjct: 221 TPSSPGIATFSHPEHTESHDPVSSTYEPQGMNSTDSNSTASVRTKVPKSDIQEETVPDNTS 280

Query: 281 SARGKEDVNKTLPNLQVVNHQQGPHHRHILKLLP-SMEATGGEKSSTPIKGPGRGHPQRN 339
 S GKE N+TLPN + HQQGPHHRHILKLLP SMEAT GEKSST IK PKRGHPRQN
 Sbjct: 281 STSGKESTNRNLTLPNPPQLTHQQGPHHRHILKLLPSSMEAT-GEKSSTAIKAPKRGHPRQN 339

Query: 340 LHKHFDINEHLPWMXXXXXXXXXXXXXXXXXCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMT 399
 HKHFDINEHLPWM CSIRKSSRTLKKGPRQDPSAI+EKAGLKKS+T
 Sbjct: 340 PHKHFDINEHLPWMIVLFLLLVLVLIVVCSIRKSSRTLKKGPRQDPSAIMEKAGLKKSMT 399



Query: 400 PTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERA 459
 PTQNREKWIYY NGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERA
 Sbjct: 400 PTQNREKWIYYRNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERA 459

Query: 460 YAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQLETDKLALXXXXXXXX 519
 YAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQLETDKLAL
 Sbjct: 460 YAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPSPLS 519

Query: 520 XXXXXXNAKLENSALLTVEPSPQDKNGFFVDESEPLLRCXXXXXXXXXXXXXXXXFITK 579
 N KLENS LLTVEPSP DKNKGFFVDESEPLLRC FITK
 Sbjct: 520 PSPIPSPNVKLENSTLLTVEPSPDKNGFFVDESEPLLRCSTSSGSSALSRNGSFITK 579

Query: 580 EKKDITVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEA 639
 EKKDITVLRQVRLDPCDLQPIFDDMLH LNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEA
 Sbjct: 580 EKKDITVLRQVRLDPCDLQPIFDDMLHILNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEA 639

Query: 640 SQTL LDSVYSHLPDLL 655
 SQTL LDSVYSHLPDLL
 Sbjct: 640 SQTL LDSVYSHLPDLL 655

 >gi|11559850|gb|AAG38115.1|  DR6 [Mus musculus]
 Length = 655

Score = 982 bits (2539), Expect = 0.0

Identities = 505/616 (81%), Positives = 519/616 (84%), Gaps = 2/616 (0%)

Query: 41 AQPEQKASNLIGTYRHVDRTGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHE 100
 AQPEQK +L GTYRHVDRTGQVLTCDKCPAGTYVSEHCTN SLRVCSSCP GTFTTRHE
 Sbjct: 41 AQPEQKTLSLPGTYRHVDRTGQVLTCDKCPAGTYVSEHCTNMSLRVCSSCPAGTFTTRHE 100

Query: 101 NGIEKCHDCSQPCPWPMEIKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVKKG 160
 NGIE+CHDCSQPCPWPMEI+LPCAALTDREC CPPGM+QSN TCAPHTVCPVGWGVKKG
 Sbjct: 101 NGIERCHDCSQPCPWPMEIERLPCAALTDRECICPPGMYQNGTCAPHTVCPVGWGVKKG 160

Query: 161 TETEDVRCKQCARGTFSDVPSSVMCKAYTDCLSNLVVVKPGTKETDNVCGTLXXXXXX 220
 TE EDVRCKQCARGTFSDVPSSVMCKA+TDCL QNL V+KPGTKETDNVCG
 Sbjct: 161 TENEDVRCKQCARGTFSDVPSSVMCKAHTDCLGQNLVVKPGTKETDNVCGMRLFFSST 220

Query: 221 XXXXXGTAIFRPEHMETHEVFSSTYVPKGMNSTESNSSASVRPKVLSSIQEGTVPDNTS 280
 GT F PEHME+H+V SSTY P+GMNST+SNS+ASVR KV S I+EGTVPDNTS
 Sbjct: 221 NPPSSGTVTFSHPEHMESHVPSSTYEPQGMNSTDSNSTASVRTKVPSPGIEEGTVPDNTS 280

Query: 281 SARGKEDVNKTLPLNLQVVNHQQGPHHRHILKLLP-SMEATGGEKSSTPIKPKRGHPRQN 339
 S GKE N+TLPLN V HQQ PHHRHILKLLP SMEAT GEKSST IK PKRGHPRQN
 Sbjct: 281 STSGKEGTNRTPNPPQVTHQQAPHHRHILKLLPSSMEAT-GEKSSTAIKAPKRGHPRQN 339

Query: 340 LHKHFDINEHLPWMXXXXXXXXXXXXXXXXXCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMT 399
 HKHFDINEHLP M CSIRKSSRTLKKGPRQDPSAIVEKAGLKKS+T
 Sbjct: 340 AHKHFDINEHLPMLMIVLFLLLVLVLIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMT 399



Query: 400 PTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERA 459
 PTQNREKWIYY NGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERA
 Sbjct: 400 PTQNREKWIYYRNGHGIDILKLVAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERA 459

Query: 460 YAALQHWITIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQLETDKLALXXXXXXXXX 519
YAALQHWITIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQLETDKLAL
Sbjct: 460 YAALQHWITIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQLETDKLALPMSPSPS 519

Query: 520 XXXXXXXXNAKLENSALLTVEPSPQDKNKGFFVDESEPLLRCDXXXXXXXXXXXXXXFITK 579
N KLENS LLTVEPSP DKNK FFVDESEPLLRCDFITK
Sbjct: 520 PSPMPSPNVKLENSTLLTVEPSPDKNKCFFVDESEPLLRCSTSSGSSALSRNGSFITK 579

Query: 580 EKKD TVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEA 639
EKKD TVLRQVRLDPCDLQPIFDDMLH LNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEA
Sbjct: 580 EKKD TVLRQVRLDPCDLQPIFDDMLHILNPEELRVIEEIPQAEDKLDRLFEIIGVKSQEA 639

Query: 640 SQTLLDSVYSHLPDLL 655
SQTLLDSVYSHLPDLL
Sbjct: 640 SQTLLDSVYSHLPDLL 655

 >gi|26329207|dbj|BAC28342.1|  unnamed protein product [Mus musculus]
Length = 573

Score = 913 bits (2359), Expect = 0.0

Identities = 468/573 (81%), Positives = 481/573 (83%), Gaps = 2/573 (0%)

Query: 84 SLRVCSSCPVGTFRHENGIEKCHDCSQPCPWPMIEKLPAAALTDRECTCPPGMFQSNAT 143
SLRVCSSCP GTFRHENGIE+CHDCSQPCPWPMIE+LPCAALTDREC CPPGM+QSN T
Sbjct: 2 SLRVCSSCPAGTFRHENGIERCHDCSQPCPWPMIERLPCAALTDRECICPPGMYQSNGT 61

Query: 144 CAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKCKAYTDCLSQNLVVIKPG 203
CAPHTVCPVGWGVRRKGTEDVRCKQCARGTFSDVPSSVMKCKA+TDCL QNL V+KPG
Sbjct: 62 CAPHTVCPVGWGVRRKGTENEDVRCKQCARGTFSDVPSSVMKCKAHTDCLGQNLVVKPG 121

Query: 204 TKETDNVCGTLXXXXXXXXXXGTAIFPRPEHMETHEVFSSTYVPKGMNSTESNSSASVR 263
TKETDNVCG GT F PEHME+H+V S TY P+GMNST+SNS+ASVR
Sbjct: 122 TKETDNVCGMRLFFSSTNPPSSGTVTFSHPEHMEHDVPSPTYEPQGMNSTDSNSTASVR 181

Query: 264 PKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVHQQPHHRHILKLLP-SMEATGGE 322
KV S I+EGTVPDNTSS GKE N+TLPN V HQQ PHHRHILKLLP SMEAT GE
Sbjct: 182 TKVPSGIEEGTVPDNTSSSTSGKEGTNRTPNPVTHQQAPHHRHILKLLPSSMEAT-GE 240

Query: 323 KSSTPIKGPGRGHPRQNLHKHFDINEHLPWMXXXXXXXXXXXXXXXXCSIRKSSRTLKKGPR 382
KSST IK PKRGHPRQN HKHFDINEHLPWM CSIRKSSRTLKKGPR
Sbjct: 241 KSSTAIKAPKRGHPRQNAHKHFDINEHLPWMIVLFLLLVLVLIVVCSIRKSSRTLKKGPR 300

Query: 383 QDPSAIVEKAGLKKSMPTQNRKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNASE 442
QDPSAIVEKAGLKKSTPTQNRKWIYY NCHGIDILKLVAQVGSQWKDIYQFLCNASE
Sbjct: 301 QDPSAIVEKAGLKKSLTPTQNRKWIYYRNGHGIDILKLVAQVGSQWKDIYQFLCNASE 360

Query: 443 REVAAFSNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTT 502
REVAAFSNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTT
Sbjct: 361 REVAAFSNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTT 420

Query: 503 QLETDKLALXXXXXXXXXXXXXXXXNAKLENSALLTVEPSPQDKNKGFFVDESEPLLRCDX 562
QLETDKLAL N KLENS LLTVEPSP DKNK FFVDESEPLLRCDFITK
Sbjct: 421 QLETDKLALPMSPSPSPMPSPNVKLENSTLLTVEPSPDKNKCFFVDESEPLLRCDS 480

Query: 563 XXXXXXXXXXXXXFITKEKKD TVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAE 622
FITKEKKD TVLRQVRLDPCDLQPIFDDMLH LNPEELRVIEEIPQAE
Sbjct: 481 TSSGSSALSRNGSFITKEKKD TVLRQVRLDPCDLQPIFDDMLHILNPEELRVIEEIPQAE 540